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RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/10/027,059A

TIME: 12:02:46

Input Set : A:\955-12.txt

Output Set: N:\CRF3\04162002\J027059A.raw

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3 <110> APPLICANT: Basson, Craig
5 <120> TITLE OF INVENTION: Transcription Factors that Regulate Normal and Malignant
Cell Growth
7 <130> FILE REFERENCE: 955-12P
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/027,059A
C--> 9 <141> CURRENT FILING DATE: 2002-04-04
9 <160> NUMBER OF SEQ ID NOS: 15
11 <170> SOFTWARE: PatentIn version 3.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 349
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
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22 Pro Asp Ala Lys Asp Leu Pro Cys Asp Ser Lys Pro Glu Ser Ala Leu
23 20 25 30
25 Gly Ala Pro Ser Lys Ser Pro Ser Pro Gln Ala Ala Phe Thr Gln
26 35 40 45
28 Gln Gly Met Glu Gly Ile Lys Val Phe Leu His Glu Arg Glu Leu Trp
29 50 55 60
31 Leu Lys Phe His Glu Val Gly Thr Glu Met Ile Ile Thr Lys Ala Gly
32 65 70 75 80
34 Arg Arg Met Phe Pro Ser Tyr Lys Val Lys Val Thr Gly Leu Asn Pro
35 85 90 95
37 Lys Thr Lys Tyr Ile Leu Leu Met Asp Ile Val Pro Ala Asp Asp His
38 100 105 110
40 Arg Tyr Lys Phe Ala Asp Asn Lys Trp Ser Val Thr Gly Lys Ala Glu
41 115 120 125
43 Pro Ala Met Pro Gly Arg Leu Tyr Val His Pro Asp Ser Pro Ala Thr
44 130 135 140
46 Gly Ala His Trp Met Arg Gln Leu Val Ser Phe Gln Lys Leu Lys Leu
47 145 150 155 160
49 Thr Asn Asn His Leu Asp Pro Phe Gly His Ile Ile Leu Asn Ser Met
50 165 170 175
52 His Lys Tyr Gln Pro Arg Leu His Ile Val Lys Ala Asp Glu Asn Asn
53 180 185 190
55 Gly Phe Gly Ser Lys Asn Thr Ala Phe Cys Thr His Val Phe Pro Glu
56 195 200 205
58 Thr Ala Phe Ile Ala Val Thr Ser Tyr Gln Asn His Lys Ile Thr Gln
59 210 215 220
61 Leu Lys Ile Glu Asn Asn Pro Phe Ala Lys Gly Phe Arg Gly Ser Asp
62 225 230 235 240
64 Asp Met Glu Leu His Arg Met Ser Arg Met Gln Ser Lys Glu Tyr Pro

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65          245          250          255
67 Val Val Pro Arg Ser Thr Val Arg Gln Lys Val Ala Ser Asn His Ser
68          260          265          270
70 Pro Phe Ser Ser Glu Ser Arg Ala Leu Ser Thr Ser Ser Asn Leu Gly
71          275          280          285
73 Ser Gln Tyr Gln Cys Glu Asn Gly Val Ser Gly Pro Ser Gln Asp Leu
74          290          295          300
76 Leu Pro Pro Pro Asn Pro Tyr Pro Leu Pro Gln Glu His Ser Gln Ile
77 305          310          315          320
79 Tyr His Cys Thr Lys Arg Lys Gly Glu Cys Asp His Pro Trp Ser Ile
80          325          330          335
82 Cys Phe Leu Ser Tyr Leu Phe Leu Ser Leu Gly Trp Gly
83          340          345
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 1050
87 <212> TYPE: DNA
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 2
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93 gacctgccct gcgattcgaa acccgagagc gcgctcgggg cccccagcaa gtccccgtcg 120
95 tccccgcagg ccgccttcac ccagcagggc atggagggaa tcaaagtgtt tctccatgaa 180
97 agagaactgt ggctaaaatt ccacgaagtg ggcacggaaa tgatcataac caaggctgga 240
99 aggcggatgt ttcccagtta caaagtgaag gtgacggggc ttaatcccaa aacgaagtac 300
101 attctttctca tggacattgt acctgccgac gatcacagat acaaattcgc agataataaa 360
103 tgggtctgtga cgggcaaaagc tgagcccgcc atgcctggcc gcctgtacgt gcacccagac 420
105 tccccgcgca ccggggcgca ttggatgagg cagctcgtct ccttccagaa actcaagctc 480
107 accaacaacc acctggaccc atttgggcat attattctaa attccatgca caaataccag 540
109 cctagattac acatcgtgaa agcggatgaa aataatggat ttggctcaaa aaatacagcg 600
111 ttctgcactc acgtctttcc tgagactgcg tttatagcag tgacttccta ccagaaccac 660
113 aagatcacgc aattaaagat tgagaataat ccctttgcca aaggatttcg gggcagtgat 720
115 gacatggagc tgcacagaat gtcaagaatg caaagtaaag aatatcccggt ggtccccagg 780
117 agcaccgtga ggcaaaaagt ggcctccaac cacagtcctt tcagcagcga gtctcgagct 840
119 ctctccacct catccaattt ggggtcccaa taccagtgtg agaatggtgt ttccggcccc 900
121 tcccaggacc tctgcctcc acccaaccca taccactgc cccaggagca tagccaaatt 960
123 taccattgta ccaagaggaa aggtgagtgt gatcacccct ggtcaatttg ctttctttct 1020
125 taccttttcc ttctcttggg ttgggggtga 1050
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129 <211> LENGTH: 518
130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 3
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137 Pro Asp Ala Lys Asp Leu Pro Cys Asp Ser Lys Pro Glu Ser Ala Leu
138          20          25          30
140 Gly Ala Pro Ser Lys Ser Pro Ser Ser Pro Gln Ala Ala Phe Thr Gln
141          35          40          45
143 Gln Gly Met Glu Gly Ile Lys Val Phe Leu His Glu Arg Glu Leu Trp
144          50          55          60

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146 Leu Lys Phe His Glu Val Gly Thr Glu Met Ile Ile Thr Lys Ala Gly
147 65 70 75 80
149 Arg Arg Met Phe Pro Ser Tyr Lys Val Lys Val Thr Gly Leu Asn Pro
150 85 90 95
152 Lys Thr Lys Tyr Ile Leu Leu Met Asp Ile Val Pro Ala Asp Asp His
153 100 105 110
155 Arg Tyr Lys Phe Ala Asp Asn Lys Trp Ser Val Thr Gly Lys Ala Glu
156 115 120 125
158 Pro Ala Met Pro Gly Arg Leu Tyr Val His Pro Asp Ser Pro Ala Thr
159 130 135 140
161 Gly Ala His Trp Met Arg Gln Leu Val Ser Phe Gln Lys Leu Lys Leu
162 145 150 155 160
164 Thr Asn Asn His Leu Asp Pro Phe Gly His Ile Ile Leu Asn Ser Met
165 165 170 175
167 His Lys Tyr Gln Pro Arg Leu His Ile Val Lys Ala Asp Glu Asn Asn
168 180 185 190
170 Gly Phe Gly Ser Lys Asn Thr Ala Phe Cys Thr His Val Phe Pro Glu
171 195 200 205
173 Thr Ala Phe Ile Ala Val Thr Ser Tyr Gln Asn His Lys Ile Thr Gln
174 210 215 220
176 Leu Lys Ile Glu Asn Asn Pro Phe Ala Lys Gly Phe Arg Gly Ser Asp
177 225 230 235 240
179 Asp Met Glu Leu His Arg Met Ser Arg Met Gln Ser Lys Glu Tyr Pro
180 245 250 255
182 Val Val Pro Arg Ser Thr Val Arg Gln Lys Val Ala Ser Asn His Ser
183 260 265 270
185 Pro Phe Arg Ser Glu Ser Arg Ala Leu Ser Thr Ser Ser Asn Leu Gly
186 275 280 285
188 Ser Gln Tyr Gln Cys Glu Asn Gly Val Ser Gly Pro Ser Gln Asp Leu
189 290 295 300
191 Leu Pro Pro Pro Asn Pro Tyr Pro Leu Pro Gln Glu His Ser Gln Ile
192 305 310 315 320
194 Tyr His Cys Thr Lys Arg Lys Glu Glu Glu Cys Ser Thr Thr Asp His
195 325 330 335
197 Pro Tyr Lys Lys Pro Tyr Met Glu Thr Ser Pro Ser Glu Glu Asp Ser
198 340 345 350
200 Phe Tyr Arg Ser Ser Tyr Pro Gln Gln Gln Gly Leu Gly Ala Ser Tyr
201 355 360 365
203 Arg Thr Glu Ser Ala Gln Arg Gln Ala Cys Met Tyr Ala Ser Ser Ala
204 370 375 380
206 Pro Pro Ser Glu Pro Val Pro Ser Leu Glu Asp Ile Ser Cys Asn Thr
207 385 390 395 400
209 Trp Pro Ser Met Pro Ser Tyr Ser Ser Cys Thr Val Thr Thr Val Gln
210 405 410 415
212 Pro Met Asp Arg Leu Pro Tyr Gln His Phe Ser Ala His Phe Thr Ser
213 420 425 430
215 Gly Pro Leu Val Pro Arg Leu Ala Gly Met Ala Asn His Gly Ser Pro
216 435 440 445
218 Gln Leu Gly Glu Gly Met Phe Gln His Gln Thr Ser Val Ala His Gln

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219      450      455      460
221 Pro Val Val Arg Gln Cys Gly Pro Gln Thr Gly Leu Gln Ser Pro Gly
222 465      470      475      480
224 Thr Leu Gln Pro Pro Glu Phe Leu Tyr Ser His Gly Val Pro Arg Thr
225      485      490      495
227 Leu Ser Pro His Gln Tyr His Ser Val His Gly Val Gly Met Val Pro
228      500      505      510
230 Glu Trp Ser Asp Asn Ser
231      515
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 1557.
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 4
239 atggccgacg cagacgaggg ctttggcctg gcgcacacgc ctctggagcc tgacgcaaaa      60
241 gacctgccct gcgattcgaa acccgagagc gcgctcgggg cccccagcaa gtccccgtcg      120
243 tccccgcagg ccgccttcac ccagcagggc atggagggaa tcaaagtgtt tctccatgaa      180
245 agagaactgt ggctaaaatt ccacgaagtg ggcacggaaa tgatcataac caaggctgga      240
247 aggcgatgt ttcccagtta caaagtgaag gtgacggggc ttaatcccaa aacgaagtac      300
249 attcttctca tggacattgt acctgccgac gatcacagat acaaattcgc agataataaa      360
251 tggctctgtg cgggcaaagc tgagcccgcc atgcctggcc gcctgtacgt gcaccagac      420
253 tcccccgcca ccggggcgca ttggatgagg cagctcgtct ccttccagaa actcaagctc      480
255 accaacaacc acctggaccc atttgggcat attattctaa attccatgca caaataccag      540
257 cctagattac acatcgtgaa agcggatgaa aataatggat ttggctcaaa aaatacagc      600
259 ttctgcactc acgtctttcc tgagactgcg tttatagcag tgacttccta ccagaaccac      660
261 aagatcacgc aattaaagat tgagaataat ccctttgcca aaggatttcg gggcagtgat      720
263 gacatggagc tgcacagaat gtcaagaatg caaagtaaa aatatcccg tggccccagg      780
265 agcaccgtga ggcaaaaagt ggccccaac cacagtcctt tcagcagcga gtctcgagct      840
267 ctctccacct catccaattt ggggtcccaa taccagtgtg agaatggtgt ttccggcccc      900
269 tcccaggacc tctgcctcc acccaacca taccactgc cccaggagca tagccaaatt      960
271 taccattgta ccaagaggaa agaggaagaa tgttccacca cagaccatcc ctataagaag      1020
273 ccctacatgg agacatcacc cagtgaagaa gattccttct accgctctag ctatccacag      1080
275 cagcagggcc tgggtgcctc ctacaggaca gagtcggcac agcggcaagc ttgcatgtat      1140
277 gccagctctg cgcccccag cgagcctgtg cccagcctag aggacatcag ctgcaacacg      1200
279 tggccaagca tgccttceta cagcagctgc accgtcacca ccgtgcagcc catggacagg      1260
281 ctaccctacc agcacttctc cgctcacttc acctcggggc ccctgggtccc tcggctggct      1320
283 ggcattggca accatggctc cccacagctg ggagagggaa tgttccagca ccagacctcc      1380
285 gtggcccacc agcctgtggt caggcagtgt gggcctcaga ctggcctgca gtcccctggc      1440
287 acccttcagc cccctgagtt cctctactct catggcgtgc caaggactct atcccctcat      1500
289 cagtaccact ctgtgcacgg agttggcatg gtgccagagt ggagcgacaa tagctaa      1557
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293 <211> LENGTH: 19
294 <212> TYPE: PRT
C--> 295 <213> ORGANISM: Artificial
297 <220> FEATURE:
298 <223> OTHER INFORMATION: synthetic peptide
300 <400> SEQUENCE: 5
301 Arg Gln Lys Val Ala Ser Asn His Ser Pro Phe Ser Ser Glu Ser Arg
302 1      5      10      15

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304 Ala Leu Cys
307 <210> SEQ ID NO: 6
308 <211> LENGTH: 29
309 <212> TYPE: DNA
C--> 310 <213> ORGANISM: Artificial
312 <220> FEATURE:
313 <223> OTHER INFORMATION: synthesized primer
315 <400> SEQUENCE: 6
316 cataaccaag gctagaaggc ggatgtttc 29
319 <210> SEQ ID NO: 7
320 <211> LENGTH: 29
321 <212> TYPE: DNA
C--> 322 <213> ORGANISM: Artificial
324 <220> FEATURE:
325 <223> OTHER INFORMATION: synthetic sequence
327 <400> SEQUENCE: 7
328 gaaacatccg ccttctagcc ttggttatg 29
331 <210> SEQ ID NO: 8
332 <211> LENGTH: 35
333 <212> TYPE: DNA
C--> 334 <213> ORGANISM: Artificial
336 <220> FEATURE:
337 <223> OTHER INFORMATION: synthetic sequence
339 <400> SEQUENCE: 8
340 gggagcgcgcg gtaatacgac tcactataga accgc 35
343 <210> SEQ ID NO: 9
344 <211> LENGTH: 33
345 <212> TYPE: DNA
C--> 346 <213> ORGANISM: Artificial
348 <220> FEATURE:
349 <223> OTHER INFORMATION: synthetic sequence
351 <400> SEQUENCE: 9
352 ggttctatag tgagtcgtat tacgcgcgct ccc 33
355 <210> SEQ ID NO: 10
356 <211> LENGTH: 27
357 <212> TYPE: DNA
C--> 358 <213> ORGANISM: Artificial
360 <220> FEATURE:
361 <223> OTHER INFORMATION: synthetic sequence
363 <400> SEQUENCE: 10
364 gaaatcactc ccaattaacg cgcgaat 27
367 <210> SEQ ID NO: 11
368 <211> LENGTH: 31
369 <212> TYPE: DNA
C--> 370 <213> ORGANISM: Artificial
372 <220> FEATURE:
373 <223> OTHER INFORMATION: synthetic sequence
375 <400> SEQUENCE: 11
376 ctagattcgc gcgttaattg ggagtgattt c 31

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/16/2002
PATENT APPLICATION: US/10/027,059A TIME: 12:02:47

Input Set : A:\955-12.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15